



United States Patent and Trademark Office

UNITED STATES DEPARTMENT OF COMMERCE United States Patent and Trademark Office Address: COMMISSIONER FOR PATENTS P.O. Box 1450 Alexandria, Virginia 22313-1450 www.uspto.gov

CONFIRMATION NO. ATTORNEY DOCKET NO. FIRST NAMED INVENTOR FILING DATE APPLICATION NO. 3914 012627-023 Frank Roesl 07/06/2001 09/899,276 EXAMINER 03/24/2004 21839 7590 ANGELL, JON E BURNS DOANE SWECKER & MATHIS L L P POST OFFICE BOX 1404 PAPER NUMBER ART UNIT ALEXANDRIA, VA 22313-1404 1635

DATE MAILED: 03/24/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

_
- 1
7
~~
, 2 2
(7

Office Action Summary

Application No.	Applicant(s)	Applicant(s)	
09/899,276	ROESL ET AL.		
Examiner	Art Unit		
J. Eric Angell	1635		

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE $\underline{3}$ MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed
- after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.

 If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.

Δnvi	re to reply within the set or extended period for repl reply received by the Office later than three months ed patent term adjustment. See 37 CFR 1.704(b).	y will, by statute, cause the applic after the mailing date of this comi	ation to become ABANDONED (35 0.5.0. § 135). munication, even if timely filed, may reduce any		
Status					
1)⊠	Responsive to communication(s) fil	ed on <u>23 December 20</u>	<u>03</u> .		
2a)□	This action is FINAL.	2b) This action is no	n-final.		
3)	Since this application is in condition	n for allowance except f	or formal matters, prosecution as to the merits is		
	closed in accordance with the prac	tice under <i>Ex parte Qua</i>	yle, 1935 C.D. 11, 453 O.G. 213.		
Disposit	ion of Claims				
4)⊠	Claim(s) 1-15 is/are pending in the	application.			
	4a) Of the above claim(s) 11-15 is/a	are withdrawn from cons	sideration.		
5)[Claim(s) is/are allowed.				
	Claim(s) <u>1-10</u> is/are rejected.				
7)	7) Claim(s) is/are objected to.				
8)[Claim(s) are subject to restr	riction and/or election re	quirement.		
Applicat	tion Papers				
 9) The specification is objected to by the Examiner. 10) The drawing(s) filed on 06 July 2001 is/are: a) accepted or b) objected to by the Examiner. Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a). Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d). 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152. 					
	under 35 U.S.C. § 119				
12)区	Acknowledgment is made of a clair	m for foreign priority und	ler 35 U.S.C. § 119(a)-(d) or (f).		
a)⊠ All b)□ Some * c)□ None of:				
	 Certified copies of the priori 	ty documents have bee	n received.		
	2. Certified copies of the priori	ty documents have been	n received in Application No		
	3. Copies of the certified copies of the priority documents have been received in this National Stage				
	application from the Interna				
*	See the attached detailed Office ac	tion for a list of the certi-	led copies not received.		
Attachma					
Attachme	ent(s) tice of References Cited (PTO-892)		4) Interview Summary (PTO-413)		
2) No	tice of Draftsperson's Patent Drawing Review	v (PTO-948)	Paper No(s)/Mail Date 5) Notice of Informal Patent Application (PTO-152)		
3) 🔀 Info	ormation Disclosure Statement(s) (PTO-1449 per No(s)/Mail Date 🚜 🐠 🌹	or PTO/SB/08)	6) Other: Notice of Informal Patent Application (PTO-132)		

Art Unit: 1635

DETAILED ACTION

1. This Action is in response to the communication filed on 12/23/01. The amendment has been entered. Claims 1-15 are currently pending in the application and are addressed herein.

Election/Restrictions

- 2. Applicant's election with traverse of Group I, claims 1-10, and further election of the species transcription factor AP-1 in the Paper filed 12/23/03 is acknowledged. The traversal is on the ground(s) that examination of all claims can be done without a serious search burden. This is not found persuasive because the three different Groups set forth in the previous election requirement indicated that each Group was classified in a different Class and/or subclass, prima facie evidence of search burden. Specifically, Group I is classified in class 435, subclass 320.1; Group II is classified in class 514, subclass 2; and Group III is classified in class 514, subclass 44. Since the different Groups have different classifications/subclassifications, this is prima facie evidence of a serious search burden, as the examiner would be required to search the different classes and subclasses for each Group.
- 3. Applicants also argue that Groups I and II are linked by linking claims and that should the elected product claims be allowable, the method claims must be rejoined. In response, it is acknowledged that should different Groups be linked by proper linking claims, then when the elected product claims are found allowable, the linked methods claims would be rejoined. However, in the instant case, Groups I and II are not linked by proper linking claims. Group I is drawn to a nucleic acid/vector and host cell while Group II is drawn to pharmaceutical compositions comprising compounds that are capable of regulating the expression of the MCP-1

Art Unit: 1635

gene by interacting with the nucleic acid of Group I. These Groups are not linked by proper linking claims because proper linking claims encompass claims drawn to products and methods of making and using the product. Here Group I is a product and Group II is a different product.

4. It is noted, however, that Group I and Group III are linked as a product and a method of using the product, and as such, should the claims of Group I be found allowable, Group III will be rejoined with Group I, ONLY as set forth in In re Ochiai, indicated below.

The examiner has required restriction between product and process claims. Where applicant elects claims directed to the product, and a product claim is subsequently found allowable, withdrawn process claims that depend from or otherwise include all the limitations of the allowable product claim will be rejoined in accordance with the provisions of MPEP § 821.04. **Process claims that depend from or otherwise include all the limitations of the patentable product** will be entered as a matter of right if the amendment is presented prior to final rejection or allowance, whichever is earlier. Amendments submitted after final rejection are governed by 37 CFR 1.116; amendments submitted after allowance are governed by 37 CFR 1.312.

In the event of rejoinder, the requirement for restriction between the product claims and the rejoined process claims will be withdrawn, and the rejoined process claims will be fully examined for patentability in accordance with 37 CFR 1.104. Thus, to be allowable, the rejoined claims must meet all criteria for patentability including the requirements of 35 U.S.C. 101, 102, 103, and 112. Until an elected product claim is found allowable, an otherwise proper restriction requirement between product claims and process claims may be maintained. Withdrawn process claims that are not commensurate in scope with an allowed product claim will not be rejoined. See "Guidance on Treatment of Product and Process Claims in light of *In re Ochiai, In re Brouwer* and 35 U.S.C. § 103(b)," 1184 O.G. 86 (March 26, 1996). Additionally, in order to retain the right to rejoinder in accordance with the above policy, Applicant is advised that the process claims should be amended during prosecution either to maintain dependency on the product claims or to otherwise include the limitations of the product claims. Failure to do so may result in a loss of the right to rejoinder.

Further, note that the prohibition against double patenting rejections of 35 U.S.C. 121 does not apply where the restriction requirement is withdrawn by the examiner before the patent issues. See MPEP § 804.01.

Art Unit: 1635

Furthermore, Applicants argue that the election of species "further limits any search burden". This is not found persuasive because a serious search burden still exists as evidenced by the fact that different classes/subclasses would have to be searched for each Group, regardless of the elected species.

Additionally, Applicants argue that Group III is classed with Group II and that Group III is also linked to Group I. With respect to the classifications of Group II and Group III, as indicated above, these Groups have different subclassifications, prima facie evidence of a serious search burden. With respect to Groups I and III being linked, it is acknowledged, as indicated above, that should the product claims (Group I) be found allowable, and only if all of the withdrawn process claims (Group III) are commensurate in scope with the allowed product, then Groups I and III (but not Group II) will be rejoined.

The requirement is still deemed proper at this time, and therefore is made FINAL.

5. Claims 11-15 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected Group, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the Paper filed 12/23/03.

Sequence Compliance

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent

Art Unit: 1635

Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) in response to this Office Action in order to avoid ABANDONMENT.

Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Applicant is requested to return a copy of the attached Notice to Comply with the response, if necessary.

It is noted that the specification contains sequences such as those disclosed on pages 5, 14, 18, 22, Figure 6, claim 2 and claim 3 that must be assigned appropriate Sequence identifiers (SEQ ID NOS.). Additionally, these sequences need to be present on a separate paper sequence listing and CRF. It appears that the sequence of claim 2 is the sequence of SEQ ID NO. 1 and the sequence of claim 3 is SEQ ID NO. 8. Therefore, the sequence errors have not precluded examination of the instant claims. However, in response to the instant Office Action, applicants must amend the specification (including claims 2 and 3) such that the disclosed sequences are assigned the appropriate SEQ ID NO. If additional sequence identifiers are required, then a new paper sequence listing as well as a new CRF will also be required. However, if the amendment merely requires adding SEQ ID NOS to the specification/claims/figure wherein the SEQ ID NOS. are already present on the sequence listing and CRF, then submission of a new CRF/sequence listing is not required.

Claim Rejections - 35 USC § 101

6. 35 U.S.C. 101 reads as follows:

Art Unit: 1635

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-6 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. The instant claims are deemed to be drawn to non-statutory subject matter because the claims encompass a naturally occurring nucleic acid molecule that comprises the limitations of claim 1, such as a naturally occurring human chromosome 17 in a human cell. That is, since the claims are not explicitly drawn to an <u>isolated</u> nucleic acid molecule, the claims must encompass naturally occurring nucleic acid molecules, such as human chromosome 17 in its natural state (i.e., in a human cell in a human body).

It is noted that amending claim 1 to indicate that the nucleic acid is an isolated nucleic acid molecule (in line 1), would obviate this rejection.

Claim Rejections - 35 USC § 112

- 7. The following is a quotation of the first paragraph of 35 U.S.C. 112:
 - The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.
- 8. Claims 1-10 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Art Unit: 1635

The Written Description Guidelines for examination of patent applications indicates, "the written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by actual reduction to practice, or by disclosure of relevant, identifying characteristics, i.e. structure or other physical and/or other chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show applicant was in possession of the claimed genus." (See MPEP 2100-164)

In the instant case, claim 1 is drawn to a nucleic acid molecule comprising a nucleic acid sequence encoding a protein having the biological activity of MCP-1 (see claim 1, part (a)). As such, claim 1, and all dependent claims, encompass nucleic acid sequences which differ from the nucleic acid sequences described in the specification (i.e., the nucleic acid sequence encoding MCP-1), including variant nucleic acid sequences which are not adequately described in the specification. Considering that the claims encompass nucleic acid sequences which encode a protein having MCP-1 biological activity, the claims encompass a genus of nucleic acid sequences that is indeterminant in size, but could possibly encompass thousands of different nucleic acid sequences, considering all of possible nucleic acid sequences, including unidentified nucleic acid sequences which encode a protein having MCP-1 biological activity. It is noted that not only does the genus of molecules encompass sequence homologues, and allelic variants, but also includes functional homologues which could have completely different structures (i.e., sequence), yet have the same function.

As indicted above, the guidelines indicate that a sufficient description of a representative number of species is required, such as by "disclosure of relevant, identifying characteristics, i.e.

Art Unit: 1635

structure or other physical and/or other chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show applicant was in possession of the claimed genus." In the instant case, the specification and prior art do not describe the relevant structural, physical or chemical properties that confer the biological activity of MCP-1 to a protein. That is, the specification and prior art do not identify the minimal critical features of the molecules encompassed by the claims that are required to encode a functional MCP-1 homologue. Without a clear indication of the features (sequences) that are critical for conferring MCP-1 biological activity, the structure-function relationship of the sequences encompassed by the claims has not been adequately described. As such, one of skill in the art would not be able to readily recognize which nucleic acid sequences would be nucleic acid sequences that encode a protein having the biological activity of MCP-1. Therefore, applicants have not sufficiently described the genus of nucleic acid sequences that are encompassed by the claims. It is noted that a review of the prior art did indicated that there are at least two sequence homologues, one encoding mouse JE and another encoding human JE (e.g., see Rollins et al., MCB 1998), however, the sequence structures of these homologues which are critical to conferring the biological activity of MCP-1 to the proteins are not described. Therefore, there is an insufficient description of the nucleic acid sequences encompassed by the claims.

It is noted that claims 2-10 depend on claim 1, and thus encompass all of the limitations of claim 1. Therefore, claims 2-10 are rejected for the same reasons.

9. Additionally, claims 1-10 are also rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for:

Art Unit: 1635

A nucleic acid molecule comprising: (a) a nucleic acid sequence encoding MCP-1, the protein encoded by the nucleic acid sequence of EMBL Accession No. Y18933; and (b) and a 5'-DHSR or 3'-DHSR wherein said 5'DHSR or said 3'-DHSR comprises the nucleic acid sequence TGAGTCA, or SEQ ID NO. 8, or SEQ ID NO. 1;

does not reasonably provide enablement for the full scope of the claims—such as a nucleic acid comprising a nucleic acid sequence encoding a protein having the biological activity of MCP-1, and 5'-DHSRs or 3'DHSRs that do not explicitly comprise TGAGTCA or SEQ ID NO. 1 or SEQ ID NO. 8. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

- 10. As mentioned above, the claims encompass sequences for which there is insufficient written description provided in the specification and include sequence homologues as well as functional homologues which may have completely different structures from the disclosed sequences. Without a clear indication of the minimal critical elements that are required to confer MCP-1 biological activity to a protein, the written description requirements have not been sufficiently met. As such, one of skill in the art would not know how to make or use the claimed invention without performing an undue amount of additional experimentation in order to first properly identify a representative number of species encompassed by the claims.
- 11. Claims 1, 5 and 6 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Art Unit: 1635

As mentioned above, the Written Description Guidelines for examination of patent applications indicates, "the written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by actual reduction to practice, or by disclosure of relevant, identifying characteristics, i.e. structure or other physical and/or other chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show applicant was in possession of the claimed genus." (See MPEP 2100-164).

The instant claims are drawn to a nucleic acid as indicated in claim 1(b) wherein the hypersensitive sequences contain mutations resulting in a modified DNAse 1 hypersensitivity, S1 hypersensitivity, and/or altered interaction with a transcription factors. Therefore, the claims encompass a genus of molecules which is indeterminant in size, but could encompass thousands of different species, considering all of the mutations which could possibly result in a modifies hypersensitivity and/or interaction with transcription factors, including mutations that have yet to be identified. Since the specification and prior art does not disclose a representative number of mutations which modify DNAse I hypersensitivity, S1 hypersensitivity and/or altered interaction with transcription factors, the written description requirement has not been met.

It is noted that claims 5 and 6 depend on claim 1. Therefore, claim 1 must broadly encompass the limitations of claim 5 and 6. As such, the rejection is applicable to claims 1, 5, and 6.

12. Additionally, claims 1, 5 and 6 are also rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for:

Page 11

Application/Control Number: 09/899,276

Art Unit: 1635

A nucleic acid molecule comprising: (a) a nucleic acid sequence encoding MCP-1, the protein encoded by the nucleic acid sequence of EMBL Accession No. Y18933; and (b) and a 5'-DHSR or 3'-DHSR wherein said 5'DHSR or said 3'-DHSR comprises the nucleic acid sequence TGAGTCA, or SEQ ID NO. 8, or SEQ ID NO. 1;

13. does not reasonably provide enablement for the full scope of the claims—such as a nucleic acid comprising a nucleic acid sequence encoding a protein having the biological activity of MCP-1, and 5'-DHSRs or 3'DHSRs that have mutations that result in DNAse I hypersensitivity, S1 hypersensitivity, or altered interaction with transcription factors. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims. As mentioned above, the claims encompass mutations for which there is insufficient written description provided in the specification. Without a clear indication of the mutations that confer hypersensitivity/altered transcription factor binding, the written description requirements have not been sufficiently met. As such, one of skill in the art would not know how to make or use the claimed invention without performing an undue amount of additional experimentation in order to first properly identify a representative number of species encompassed by the claims.

It is noted that claims 5 and 6 depend on claim 1. Therefore, claim 1 must broadly encompass the limitations of claim 5 and 6. As such, the rejection is applicable to claims 1, 5, and 6.

Claim Rejections - 35 USC § 102

14. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

Art Unit: 1635

A person shall be entitled to a patent unless -

- (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
- 15. Claims 1-4 and 6-10 are rejected under 35 U.S.C. 102(b) as being anticipated by Genbank Accession No. AC005549 (Birren et al., see sequence alignment attached. NOTE: Birren is listed in the IDS PTO-1449.)
- 16. Birren (Genbank Accession No. AC005549) teaches a bacterial artificial chromosome (BAC) comprising a portion of chromosome 17 that comprises SEQ ID NO. 1, as well as the genomic DNA encoding the MCP-1 gene. The Genbank data (see attached) indicates that the sequence matching SEQ ID NO. 1 is comprised in a BAC, wherein the BAC also includes a genomic sequence encoding MCP-1. Since SEQ ID NO. 1 is the 3'DHSR nucleic acid sequence from position +2430 to +3019 as depicted in Figure 6 (see claim 2), and the genomic sequence encoding human MCP-1, the BAC taught by Birren in Genbank Accession No. AC005549 thus meets the limitations of claims 1-4. It is noted that the BAC is a recombinant vector that must include all of the genomic sequences of chromosome 17 associated with the expression of MCP-1 in human cells (i.e., the regulatory elements that allow the expression of MCP-1 in cukaryotic host cells). Furthermore, the construction of the BAC would require the transformation of the BAC into bacterial cells for the propagation of the instant BAC. As such, Birren (through Genbank Accession No. AC005549) necessarily teaches all of the limitations of the instant claims.

Art Unit: 1635

Conclusion

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to J. Eric Angell whose telephone number is (571) 272-0756. The examiner can normally be reached on M-F (8:00-5:30) with every other Friday off.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John L. LeGuyader can be reached on (571) 272-0760. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Jon Eric Angell, Ph.D. Art Unit 1635

Athehment to office Action p. see Result 4

/number=2 8968. .>9073 exon /qene="MCP-1" /number=3 ORIGIN 100.0%; Score 600; DB 9; Length 11793; Query Match Best Local Similarity 100.0%; Pred. No. 9.3e-143; 0: Mismatches 0; Indels 0; Matches 600; Conservative Gaps 1 TAGGAAAATTATAGGATCATTAAGAAAGGAGAAGGAAGAGTGGGAGCAAATACCTGGAGG 60 Qу 9979 TAGGAAATTATAGGATCATTAAGAAAGGAGAAGGAAGGAGGAGGAGCAAATACCTGGAGG 10038 Dh 61 TAGAAATGGTGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATT 120 Qу 10039 TAGAAATGGTGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATT 10098 Db Qy Db 181 AATGTTAGGGTGAAAAGTTÄCTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT 240 Qу 10159 AATGTTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT 10218 Db 241 TCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATG 300 Qу Db 301 TAACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATG 360 Qу 10279 TAACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATG 10338 Db 361 GTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATG 420 Qу 10339 GTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCCAATGAAGAATG 10398 Db 421 AGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAGACCTGTGACTTCAGA 480 QУ 10399 AGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAGACCTGTGACTTCAGA 10458 Db 481 TATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTCCCTGAAACCAGAATGT 540 Qу 10459 TATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGGCAGCTTCCCTGAAACCAGAATGT 10518 Db 541 GTTTCCCTCCATTACTATACCCCCATCCCAATCTCAGGCACCTGGAATCATCCATTTAAA 600 Qу 10519 GTTTCCCTCCATTACTATACCCCCATCCCAATCTCAGGCACCTGGAATCATCCATTTAAA Db RESULT 4 AC005549/c PRI 22-SEP-1998

LOCUS AC005549 147416 bp DNA linear PRI 22-SEP-1998 DEFINITION Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.

ACCESSION AC005549

VERSION AC005549.1 GI:3598724

```
KEYWORDS
            HTG.
            Homo sapiens (human)
SOURCE
            Homo sapiens
  ORGANISM
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                (bases 1 to 147416)
REFERENCE
             Birren, B., Linton, L., Nusbaum, C. and Lander, E.
  AUTHORS
             Homo sapiens chromosome 17, clone hRPK.215 E_13
  TITLE
             Unpublished
  JOURNAL
                (bases 1 to 147416)
REFERENCE
             Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
  AUTHORS
             Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J.,
             Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M.,
             Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E.,
             Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W.,
             Forrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G.,
             Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C.,
             Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J.,
             Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
             Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
             Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P.,
             Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A.,
             Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C.,
             Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I.,
             Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D.,
             Ye, W.J., Zhao, J. and Zody, M.
             Direct Submission
  TITLE
             Submitted (27-AUG-1998) Whitehead Institute/MIT Center for Genome
  JOURNAL
             Research, 320 Charles Street, Cambridge, MA 02141, USA
                 (bases 1 to 147416)
REFERENCE
             Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
  AUTHORS
             Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J.,
             Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M.,
             Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E.,
             Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W.,
             Forrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G.,
             Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C.,
             Jacotot,L., Jones,C., Kann,L., Karatas,A., Lehoczky,J.,
             Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
             Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
             Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P.,
             Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P.,
             Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C.,
             Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I.,
             Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D.,
             Ye, W.J., Zhao, J. and Zody, M.
             Direct Submission
   TITLE
             Submitted (12-SEP-1998) Whitehead Institute/MIT Center for Genome
   JOURNAL
             Research, 320 Charles Street, Cambridge, MA 02141, USA
                 (bases 1 to 147416)
 REFERENCE
              Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
   AUTHORS
             Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J.,
              Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M.,
              Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E.,
              Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W.,
              Forrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G.,
              Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C.,
```

```
Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J.,
          Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
          Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
          Nahf,R., Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P.,
          Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P.,
          Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C.,
          Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I.,
          Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D.,
          Ye, W.J., Zhao, J. and Zody, M.
          Direct Submission
JOURNAL
          Submitted (22-SEP-1998) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
          On Sep 13, 1998 this sequence version replaced gi:3581743.
          All repeats were identified using RepeatMasker: Smit, A.F.A. &
          Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html
          Only the first 147416 bases of this clone are being submitted.
          Bases 145417-155040 overlap accession number AC004147 (WICGR
          project L228). The first 2Kb of the overlapping region are
          submitted to confirm overlap.
                   Location/Qualifiers
   source
                   1. .147416
                   /organism="Homo sapiens"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:9606"
                   /chromosome="17"
                   /map="17"
                 /clone="hRPK.215_E_13"
                  /clone_lib="RPCI-11 human BAC library"
  repeat region
                   2. .69
                   /rpt family="BUR1"
  repeat_region
                   490. .695
                   /rpt_family="L1ME2"
                   1291. .1390
  repeat region
                   /rpt family="MIR"
  repeat region
                   2980. .3131
                   /rpt family="MER5A"
  repeat_region
                   complement (3147. .3241)
                   /rpt family="MIR"
  repeat region
                   complement (4228. .4469)
                   /rpt_family="MLT1I"
  repeat_region
                   complement (5430. .5549)
                   /rpt family="FLAM C"
  repeat region
                   complement (5941. .6051)
                   /rpt_family="MER81"
  repeat region
                   6131. .6250
                   /rpt_family="(TA)n"
                   6406. .6455
  repeat region
                   /rpt_family="AT rich"
                   6574. .6600
  repeat_region
                   /rpt_family="MLT1D"
  repeat_region
                   6601. .6880
                   /rpt_family="AluJb"
  repeat_region
                   6881. .6935
                   /rpt_family="MLT1D"
  repeat_region
                   7119. .7360
```

TITLE

COMMENT

FEATURES

```
/rpt_family="MLT1D"
repeat_region
                7337. .7636
                /rpt family="MLT1D"
                7689. .7888
repeat_region
                /rpt family="L1ME3"
                8023. .8048
repeat_region
                 /rpt_family="AT_rich"
repeat_region
                8871. .8986
                 /rpt family="MIR"
                10109. .10258
repeat_region
                 /rpt family="MER5A"
repeat_region
                complement(11031. .11072)
                /rpt_family="MIR"
                11567. .11836
repeat_region
                /rpt family="L2"
                12501. .12981
repeat_region
                /rpt_family="MER9"
                complement (12983. .13257)
repeat_region
                /rpt_family="AluJb"
                15248. .15364
repeat_region
                /rpt family="MIR"
repeat_region
                complement (16483. .16653)
                /rpt_family="MIR"
                16830. .16949
repeat_region
                /rpt_family="MER5A"
                17203. .17380
repeat region
                /rpt family="LTR16A"
                17393. .18306
repeat_region
                /rpt family="HERVL"
                18315. .24307
repeat_region
                /rpt_family="L1PA2"
repeat_region
                24309. .24335
                /rpt_family="AT_rich"
                24513. .25245
repeat_region
                /rpt family="HERVL"
                25613. .25758
repeat_region
                /rpt_family="HERVL"
                26135. .26228
repeat region
                /rpt family="LTR16A"
                complement (27814. .27950)
repeat_region
                /rpt family="MER94"
repeat_region
                28930. .28968
                /rpt_family="AT_rich"
repeat_region
                29960. .30341
                /rpt family="MLT1I"
repeat_region
                32364. .32581
                /rpt family="MIR"
repeat_region
                32601. .32902
                /rpt family="AluSx"
                complement(33593. .39359)
repeat_region
                /rpt_family="L1PA2"
repeat_region
                39362. .39414
                /rpt_family="A-rich"
repeat_region
                complement(39920. .40047)
                /rpt family="MIR"
repeat_region
                40112. .40151
                /rpt family="AT rich"
```

```
complement (40810. .40898)
    repeat region
               /rpt_family="MLT1J"
    repeat_region
               41293. .41469
               /rpt family="L1PA6"
   repeat_region
               complement (41846. .41956)
               /rpt family="purine-rich"
               complement (42486. .42569)
   repeat_region
               /rpt family="MLT1I"
               42979. .43098
   repeat region
               /rpt family="MER5A"
               43554. .43983
   repeat region
               /rpt family="LTR24"
               44781. .44811
   repeat_region
               /rpt family="AT rich"
   repeat_region
               46184. .46296
               /rpt family="MIR"
   repeat_region
               complement (47075. .47140)
               /rpt family="MLT1G"
   repeat_region
               complement (47266. .47307)
               /rpt_family="(CA)n"
   repeat_region
               complement (47363. .47442)
               /rpt family="MLT1G"
               complement (48165. .48209)
   repeat_region
 Query Match
                   100.0%; Score 600; DB 9; Length 147416;
 Best Local Similarity
                  100.0%; Pred. No. 5.5e-143;
 Matches 600; Conservative 0; Mismatches
                                    0; Indels
QУ
        1 TAGGAAAATTATAGGATCATTAAGAAAGGAGAAGGAAGAGTGGGAGCAAATACCTGGAGG 60
          Db
        61 TAGAAATGGTGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATT 120
Qу
          Db
      58974 TAGAAATGGTGATGATGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATT 58915
       Qу
          Db
       181 AATGTTAGGGTGAAAAGTTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT 240
Qу
          58854 AATGTTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT 58795
Db
       241 TCAGTCCAATGAGGAGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATG 300
QУ
          58794 TCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATG 58735
Db
Qу
       301 TAACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATG 360
          58734 TAACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATG 58675
Db
       361 GTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATG 420
Qу
          Db
     58674 GTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCCAATGAAGAATG 58615
```

complement (40152. .40442)

/rpt family="AluJo"

repeat region

```
421 AGCCATGCAGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAGACCTGTGACTTCAGA 480
Qу
             58614 AGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAGACCTGTGACTTCAGA 58555
Db
         481 TATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTCCCTGAAACCAGAATGT 540
Qу
             58554 TATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTCCCTGAAACCAGAATGT 58495
Db
         541 GTTTCCCTCCATTACTATACCCCCATCCCAATCTCAGGCACCTGGAATCATCCATTTAAA 600
Qy
             58494 GTTTCCCTCCATTACTATACCCCCATCCCAATCTCAGGCACCTGGAATCATCCATTTAAA 58435
Db
RESULT 5
HSJER
                                                   linear PRI 03-NOV-1992
                                           DNA
                                 2243 bp
LOCUS
           HSJEPR
           H.sapiens gene for JE protein, exons 3 and 4.
DEFINITYON
           X60001
ACCESSION
           X60001.1 GI:34001
VERSION
           JE protein; secretory protein.
KEYWORDS
           Homo sapiens (human)
SOURCE
           Homo sapiens
  ORGANISM
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              (bases 1 to 2243)
REFERENCE
           Schwarz, E., Fan, E., Kallin, B., Sorrentino, V. and Bloom, B.
  AUTHORS
           The IFN-gamma inducible cDNA gamma.1 is an incompletely spliced JE
  TITLE
           cDNA
           Unpublished
  JOURNAL
              (bases 1 to 2243)
REFERENCE
           Schwarz, E.
  AUTHORS
           Direct Submission
  TITLE
           Submitted (16-MAY-1991) E. Schwarz, Albert Einstein College of
  JOURNAL
           Medicine, Dept of Microbiology & Immunology, Forchheimer Bldg Room
           411, 1300 Morris Park\Avenue, Bronx NY 10461, USA
                    Location/Qual Miers
FEATURES
                    1. .2243
     source
                    /organism="Homo kapiens"
                    /mol_type="genomid DNA"
                    /db xref="taxon:9606"
                    /tissue_type="liver"
                    /clone_lib="Okayama-Barg plasmid"
                    /dev_stage="fetal"
                    <1. .612
     intron
                    /number=1
                    613. .1591
     gene
                    /gene="gamma 1,hje"
                    613. .730
     exon
                    /gene="gamma 1,hje"
                    /product="JE protein"
                    /number=2
                    731. .1112
     intron
                    /gene="gamma 1,hje"
                    /number=2
                    1113. .1591
     exon
                    /gene="gamma 1,hje"
```

Notice to Comply

Application No. 819,276 Examiner

RÖSL et al. Art Unit 1635

Applicant(s)

J. Eric Angell

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE **DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The purcleotide and/or amino acid sequence disclosure contained in this application does not comply with

the	requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):
\boxtimes	1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
	2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
	3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
	4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
	5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
	6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
	7. Other: _
	plicant Must Provide: An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
_	An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its ry into the specification .
app	A statement that the content of the paper and computer readable copies are the same and, where dicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 25(d).
Fo	r questions regarding compliance to these requirements, please contact:
Fo	r Rules Interpretation, call (703) 308-4216 or (703) 308-2923 r CRF Submission Help, call (703) 308-4212 tentIn Software Program Support
	Technical Assistance703-287-0200 To Purchase Patentln Software703-306-2600
ΡI	EASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY